VERSION WITH MARKINGS TO SHOW CLAIM CHANGES MADE

1. (Amended) A method for generating a genomic profile comprising:

a) providing[:] a sample from a perioperative subject, and

[i) a sample from a perioperative subject; and]

[ii) an assay for detecting two or more genetic markers; and]

b) subjecting said sample to [said assay]an assay for detecting two or more genetic markers to generate a genomic profile for use in selecting a perioperative course of action.

13. (Amended) A method for generating a genomic profile comprising:

a) providing[:] a sample from a perioperative subject; and

[i) a sample from a subject; and]

[ii) an assay for detecting two or more genetic markers; and]

b) subjecting said sample to [said assay] an assay for detecting two or more genetic markers to generate a genomic profile for use in selecting a surgical procedure [medical] treatment course of action.

17. (Amended) A method[,] for generating a genomic profile comprising:

a) providing a sample from a perioperative subject; and

[i) a sample from a subject; and]

[ii) an assay for detecting two or more genetic markers associated with a pharmacological response;]

b) [testing said sample in said assay] subjecting said sample to an assay for detecting two or more genetic markers associated with a pharmacological response to generate a genomic profile for use in selecting a surgical procedure treatment course of action; and

c) subjecting said subject to a surgical procedure, wherein the conditions for said procedure are based on said genomic profile.

VERSION WITH MARKINGS TO SHOW SPECIFICATION CHANGES MADE

Paragraph beginning on page 24, line 11:

Page 24, line 18, please delete "(http://www.ncbi.nlm.nih.gov/SNP/)" and add -- available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site--.

Paragraph beginning on page 26, line 21 (*i.e.*, the last paragraph on page 26 that spans pages 26 and 27):

On page 26, line 25, please delete "DbEST (http://www.ncbi.nlm.nih.gov/dbES); EBI/EMBL (http://www.ebi.ac.uk/mutations); EBI (http://www.ebi.ac.uk/ebi_home.html); EMBL (http://www.ebi.ac.uk/queries/queries.html); GDB (http://www.gdb.org/gdb/gdbtop.html); GeneCards (http://bioinformatics.weizmann.ac.il/cards/index.html); GeneClinics (http://www.geneclinics.org); Genethon (http://www.genethon.fr/genethon_en.html); GSDB (http://www.ncgr.org); HGP (http://www.ornl.gov/TechResources/Human_Genome/home.html); Human Gene Mutation Databoase (http://www.uwcm.ac.uk/uwcm/mg/search); NCBI (http://www.ncbi.nlm.nih.gov/); OMIM (http://www.ncbi.nlm.nih.gov/Omim/); PubMed (http://www.ncbi.nlm.nih.gov/PubMed/); Research Tools (NCBI) (http://www.ncbi.nlm.nih.gov/SCIENCE96/ResTools.html); RHdb (http://www.ebi.ac.uk/RHdb); Stanford Human Genome Center (http://www.shgc.stanford.edu/); HUGO (http://www.gene.ucl.ac.uk/hugo); TIGR (http://www.tigr.org/); The National Human Genome Research Institute (http://www.nhgri.nih.gov/); The Whitehead Institute Center for Genome (http://www.genome.wi.mit.edu/); Unigene (http://www.ncbi.nlm.nih.gov/Unigene/index.html); University of Oklahoma (http://www.dna1.chem.ou.edu/index.html); and WEHI (http://wehih.wehi.edu.au/srs/srs6/)."

and insert -- DbEST (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); EBI/EMBL (available at the EMBL European Bioinformatics Institute public web site); EBI (available at the EMBL European Bioinformatics Institute public web site); EMBL (available at the EMBL European Bioinformatics Institute public web site); The Genome Database (GDB) (available at Genome Database public web site); GeneCards (Rebhan *et al.*, GeneCards: encyclopedia for genes, proteins and diseases. Weizmann Institute of Science, Bioinformatics Unit and Genome Center, Rehovot, Israel, 1997); GeneClinics (GeneClinics: Clinical Genetic Information Resource [database online], Copyright, University of Washington, Seattle. 1995-, Updated weekly); Genethon (available from Human Genome Research Centre public web site); GSDB (available from the National Center for Genome Research public web site); HGP (available from the Human Genome Project public web site); Human Gene Mutation Database (available at the Human Gene Mutation Database public web site); NCBI (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); OMIM (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); PubMed (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); Research Tools (NCBI) (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); RHdb (available at the EMBL European Bioinformatics Institute public site); Stanford Human Genome Center (available at the Stanford Human Genome Center public web site); HUGO (available at the The Human Genome Organization public web site); TIGR (available at the Institute for Genomic Research public web site); The National Human Genome Research Institute (available at the National Human Genome Research Institute public web site); The Whitehead Institute Center for Genome (available at the Whitehead Institute for Biomedical Research/MIT Center for Genome Research); Unigene (available at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health web site); University of Oklahoma (available at the University of Oklahoma's Advanced Center for Genome Technology public web site); and WEHI (available at the Walter and Eliza Hall Institute of Medical Research public web site).--.

PENDING CLAIMS

1. (Amended) A method for generating a genomic profile comprising:

a) providing a sample from a perioperative subject, and

b) subjecting said sample to an assay for detecting two or more genetic markers to generate a genomic profile for use in selecting a perioperative course of action.

2. The method of Claim 1, wherein said course of action comprises administration of anesthesia during a surgical procedure.

3. The method of Claim 2, wherein said anesthesia is a general anesthesia.

4. The method of Claim 2, wherein said anesthesia is a regional anesthesia.

5. The method of Claim 2, wherein said surgical procedure is non-invasive surgery.

6. The method of Claim 2, wherein said surgical procedure is invasive surgery.

7. The method of Claim 1, wherein said course of action comprises administration of anesthesia during a medical procedure.

8. The method of Claim 1, wherein said genomic profile comprises information pertaining to a pharmacodynamic risk.

9. The method of Claim 1, wherein said genomic profile comprises information pertaining to a pharmacokinetic risk.

10. The method of Claim 1, wherein said genomic profile comprises a presymptomatic diagnosis.

11. The method of Claim 1, wherein said genomic profile comprises information pertaining to differential diagnosis of co-existing diseases.

12. The method of Claim 1, wherein said two or more genetic markers comprises a mutation in two or more genes, said genes selected from the group consisting of BChE, CYP2D6, MTHFR, MS, CBS, F 5 Leiden, Prothrombin, RYR1, CACNA1S, and CPT 2.

13. (Amended) A method for generating a genomic profile comprising:

a) providing a sample from a perioperative subject; and

b) subjecting said sample to an assay for detecting two or more genetic markers to generate a genomic profile for use in selecting a surgical procedure treatment course of action.

14. The method of Claim 13, wherein said sample is taken from said subject in a time frame selected from: prior to undergoing a medical procedure, during a medical procedure, and following a medical procedure.

15. The method of Claim 14, wherein said medical treatment is non-surgical.

16. The method of Claim 14, wherein said medical treatment is surgical.

17. (Amended) A method for generating a genomic profile comprising:

a) providing a sample from a perioperative subject; and

b) subjecting said sample to an assay for detecting two or more genetic markers associated with a pharmacological response to generate a genomic profile for use in selecting a surgical procedure treatment course of action; and

c) subjecting said subject to a surgical procedure, wherein the conditions for said procedure are based on said genomic profile.

18. The method of claim 17, wherein said pharmacological response is to an anesthetic.

19. The method of claim 18, wherein said conditions for said procedure is the choice of anesthetic.

20. The method of Claim 17, wherein said two or more genetic markers comprises a mutation in two or more genes, said genes selected from the group consisting of BChE, CYP2D6, MTHFR, MS, CBS, F 5 Leiden, Prothrombin, RYR1, CACNA1S, and CPT 2.